We claim:

1. A computerized method for designing a resequencing array to resequence a user selected sequence comprising:

receiving a user design request comprising a user selected sequence;

producing an array design for resequencing said user selected sequence;

outputting said array design to said user;

receiving acceptance for said array design from said user;

outputting a file that is useful for controlling a nucleic acid synthesizer during the construction of an array comprising said array design;

synthesizing at least one copy of said array; and

providing said at least one copy of said array to said user.

2. The method of claim 1 wherein said nucleic acid synthesizer is maskless.

3. The method of claim 1 wherein said user design request comprises a sequence file.

4. The method of claim 1 wherein said user design request is received over the internet.

5. The method of claim 1 wherein the array further comprises user selected control probes.

6. A method for a provider of nucleic acid arrays to provide a user with an array for resequencing a user selected nucleic acid wherein the method comprises:

receiving a sequence computer file from said user wherein the sequence computer file comprises the sequence of the user selected nucleic acid;

preparing a design for a resequencing array for the selected sequence;

outputting said design into a design computer file;

providing said design computer file to said user;

receiving approval for said design from said user;

outputting an instruction computer file wherein said instruction computer file provides instructions to a nucleic acid synthesizer for synthesis of an array comprising said design;

synthesizing said array; and

providing said user with said array.

7. The method of claim 6 wherein after receiving from said user said sequence computer file the provider analyzes the sequence to remove repetitive sequences.

8. The method of claim 6 wherein said provider identifies ambiguous sequence within said user selected nucleic acid sequence by: obtaining analogous sequence from at least one other source; comparing the sequence from said file to said sequence from at least one other source; identifying bases that are different and removes ambiguity by comparing the sequence from two or more sources.

9. The method of claim 6 wherein said provider provides said user with computer executable code for identifying ambiguous sequence within a selected sequence and for resolving the ambiguity of the identified ambiguous sequence.

10. The method of claim 6 wherein said provider also provides said user with the sequence of primers that may be used to amplify said user selected sequence.

11. The method of claim 10 wherein said provider further provides a graphical user interface for said user to order primers with the provided sequence from a third party on the internet.

12. The method of claim 6 wherein said user selected sequence is identified by said user in an association study or a linkage study wherein said sequence is associated with a phenotype.

13. The method of claim 6 wherein said user first identifies said user selected sequence as being associated with a phenotype using a genotyping array that genotypes more than 10,000 different human polymorphisms.

14. The method of claim 6 wherein said sequence computer file is received by the provider over the Internet.

15. The method of claim 6 wherein said design computer file is provided to the user over the Internet.

16. A method for providing resequencing arrays to a user comprising:

using a computer to design one or more resequencing arrays for one or more regions of a genome of interest;

providing users with a list of available designs for resequencing arrays;

receiving an order from a user for a specific design from said list of available designs wherein said specific design is for an array to resequence a selected sequence;

outputting an instruction computer file for said specific design to a nucleic acid synthesizer;

synthesizing an array using said instruction computer file; and

providing the array or arrays to said user.

17. The method of claim 16 further comprising providing primer sequences to the user, wherein said primer sequences may be used to amplify at least one region of said selected sequence.

18. The method of claim 16 wherein said genome of interest is the human genome.

19. The method of claim 16 wherein said selected sequence comprises at least one complete chromosome.

20. The method of claim 16 wherein said list of available designs is provided to said user over the Internet.